

RAW SEQUENCE LISTING

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Information Center (STIC) no errors detected.**

Application Serial Number: 101078,927B
Source: IFW16
Date Processed by STIC: 06-22-2005

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IFW16

RAW SEQUENCE LISTING

DATE: 06/22/2005

PATENT APPLICATION: US/10/078,927B

TIME: 17:07:57

Input Set : A:\SJ-01-0032 Revised 0305.ST25.txt

Output Set: N:\CRF4\06222005\J078927B.raw

3 <110> APPLICANT: St. Jude Children's Research Hospital
 4 St. Jude Children's Research Hospital
 5 Curran, Thomas
 6 Keshvara, Lakhu
 8 <120> TITLE OF INVENTION: Cyclin Dependent Kinase 5 Phosphorylation of Disabled 1
 Protein
 10 <130> FILE REFERENCE: SJ-01-0032
 12 <140> CURRENT APPLICATION NUMBER: 10/078,927B
 13 <141> CURRENT FILING DATE: 2002-02-19
 15 <160> NUMBER OF SEQ ID NOS: 4
 17 <170> SOFTWARE: PatentIn version 3.2
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 6
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Mus musculus
 25 <220> FEATURE:
 26 <221> NAME/KEY: DOMAIN
 27 <222> LOCATION: (1)..(6)
 28 <223> OTHER INFORMATION: smallest carboxy terminal Dab1 tryptic fragment containing a
 Cdk5
 29 phosphorylation site
 31 <220> FEATURE:
 32 <221> NAME/KEY: SITE
 33 <222> LOCATION: (3)..(3)
 34 <223> OTHER INFORMATION: Serine at residue #3 equates to Serine491 in mouse Dab1
 sequence
 35 Cdk5 phosphorylation of Serine requires a Proline (P) in the +1
 36 position and a Lysine (K) in the +3 position
 38 <400> SEQUENCE: 1
 40 Gln Ser Ser Pro Ser Lys
 41 1 5
 44 <210> SEQ ID NO: 2
 45 <211> LENGTH: 24
 46 <212> TYPE: PRT
 47 <213> ORGANISM: Mus musculus
 50 <220> FEATURE:
 51 <221> NAME/KEY: DOMAIN
 52 <222> LOCATION: (1)..(24)
 53 <223> OTHER INFORMATION: Dab1 tryptic fragment containing a Cdk5 phosphorylation site
 55 <220> FEATURE:
 56 <221> NAME/KEY: SITE
 57 <222> LOCATION: (21)..(21)
 58 <223> OTHER INFORMATION: Serine at Reisdue 21 equates to Serine515 in mouse Dab1
 sequence

59 Cdk5 phosphorylation of Serine requires a Proline (P) in the +1
60 position and a Lysine (K) in the +3 position
62 <400> SEQUENCE: 2

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64 Ser Ser Ala Ser His Val Ser Asp Pro Thr Ala Asp Asp Ile Phe Glu
65 1          5          10          15
68 Glu Gly Phe Glu Ser Pro Ser Lys
69          20
72 <210> SEQ ID NO: 3
73 <211> LENGTH: 14
74 <212> TYPE: PRT
75 <213> ORGANISM: Mus musculus
78 <220> FEATURE:
79 <221> NAME/KEY: DOMAIN
80 <222> LOCATION: (1)..(14)
81 <223> OTHER INFORMATION: Dab1 phosphopeptide domain used for antibody production
83 <220> FEATURE:
84 <221> NAME/KEY: MOD_RES
85 <222> LOCATION: (8)..(8)
86 <223> OTHER INFORMATION: PHOSPHORYLATION, equates to Serine491 in mouse Dab1 sequence
87 Cdk5 phosphorylation of Serine requires a Proline (P) in the +1
88 position and a Lysine (K) in the +3 position
90 <400> SEQUENCE: 3
92 Thr Pro Ala Pro Arg Gln Ser Ser Pro Ser Lys Ser Ser Ala
93 1          5          10
96 <210> SEQ ID NO: 4
97 <211> LENGTH: 555
98 <212> TYPE: PRT
99 <213> ORGANISM: Mus musculus
101 <400> SEQUENCE: 4
103 Met Ser Thr Glu Thr Glu Leu Gln Val Ala Val Lys Thr Ser Ala Lys
104 1          5          10          15
107 Lys Asp Ser Arg Lys Lys Gly Gln Asp Arg Ser Glu Ala Thr Leu Ile
108          20          25          30
111 Lys Arg Phe Lys Gly Glu Gly Val Arg Tyr Lys Ala Lys Leu Ile Gly
112          35          40          45
115 Ile Asp Glu Val Ser Ala Ala Arg Gly Asp Lys Leu Cys Gln Asp Ser
116          50          55          60
119 Met Met Lys Leu Lys Gly Val Val Ala Gly Ala Arg Ser Lys Gly Glu
120 65          70          75          80
123 His Lys Gln Lys Ile Phe Leu Thr Ile Ser Phe Gly Gly Ile Lys Ile
124          85          90          95
127 Phe Asp Glu Lys Thr Gly Ala Leu Gln His His His Ala Val His Glu
128          100          105          110
131 Ile Ser Tyr Ile Ala Lys Asp Ile Thr Asp His Arg Ala Phe Gly Tyr
132          115          120          125
135 Val Cys Gly Lys Glu Gly Asn His Arg Phe Val Ala Ile Lys Thr Ala
136          130          135          140
139 Gln Ala Ala Glu Pro Val Ile Leu Asp Leu Arg Asp Leu Phe Gln Leu
140 145          150          155          160
143 Ile Tyr Glu Leu Lys Gln Arg Glu Glu Leu Lys Lys Ala Gln Lys
144          165          170          175
147 Asp Lys Gln Cys Glu Gln Ala Val Tyr Gln Thr Ile Leu Glu Glu Asp

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148          180          185          190
151 Val Glu Asp Pro Val Tyr Gln Tyr Ile Val Phe Glu Ala Gly His Glu
152          195          200          205
155 Pro Ile Arg Asp Pro Glu Thr Glu Glu Asn Ile Tyr Gln Val Pro Thr
156          210          215          220
159 Ser Gln Lys Lys Glu Gly Val Tyr Asp Val Pro Lys Ser Gln Pro Val
160 225          230          235          240
163 Ser Ala Val Thr Gln Leu Glu Leu Phe Gly Asp Met Ser Thr Pro Pro
164          245          250          255
167 Asp Ile Thr Ser Pro Pro Thr Pro Ala Thr Pro Gly Asp Ala Phe Leu
168          260          265          270
171 Pro Ser Ser Ser Gln Thr Leu Pro Gly Ser Ala Asp Val Phe Gly Ser
172          275          280          285
175 Met Ser Phe Gly Thr Ala Ala Val Pro Ser Gly Tyr Val Ala Met Gly
176          290          295          300
179 Ala Val Leu Pro Ser Phe Trp Gly Gln Gln Pro Leu Val Gln Gln Gln
180 305          310          315          320
183 Ile Ala Met Gly Ala Gln Pro Pro Val Ala Gln Val Ile Pro Gly Ala
184          325          330          335
187 Gln Pro Ile Ala Trp Gly Gln Pro Gly Leu Phe Pro Ala Thr Gln Gln
188          340          345          350
191 Ala Trp Pro Thr Val Ala Gly Gln Phe Pro Pro Ala Ala Phe Met Pro
192          355          360          365
195 Thr Gln Thr Val Met Pro Leu Ala Ala Ala Met Phe Gln Gly Pro Leu
196          370          375          380
199 Thr Pro Leu Ala Thr Val Pro Gly Thr Asn Asp Ser Ala Arg Ser Ser
200 385          390          395          400
203 Pro Gln Ser Asp Lys Pro Arg Gln Lys Met Gly Lys Glu Ser Phe Lys
204          405          410          415
207 Asp Phe Gln Met Val Gln Pro Pro Pro Val Pro Ser Arg Lys Pro Asp
208          420          425          430
211 Gln Pro Ser Leu Thr Cys Thr Ser Glu Ala Phe Ser Ser Tyr Phe Asn
212          435          440          445
215 Lys Val Gly Val Ala Gln Asp Thr Asp Asp Cys Asp Asp Phe Asp Ile
216          450          455          460
219 Ser Gln Leu Asn Leu Thr Pro Val Thr Ser Thr Thr Pro Ser Thr Asn
220 465          470          475          480
223 Ser Pro Pro Thr Pro Ala Pro Arg Gln Ser Ser Pro Ser Lys Ser Ser
224          485          490          495
227 Ala Ser His Val Ser Asp Pro Thr Ala Asp Asp Ile Phe Glu Glu Gly
228          500          505          510
231 Phe Glu Ser Pro Ser Lys Ser Glu Glu Gln Glu Ala Pro Asp Gly Ser
232          515          520          525
235 Gln Ala Ser Ser Thr Ser Asp Pro Phe Gly Glu Pro Ser Gly Glu Pro
236          530          535          540
239 Ser Gly Asp Asn Ile Ser Pro Gln Asp Gly Ser
240 545          550          555

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VERIFICATION SUMMARY

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